



OSSYLISS CHOSSE

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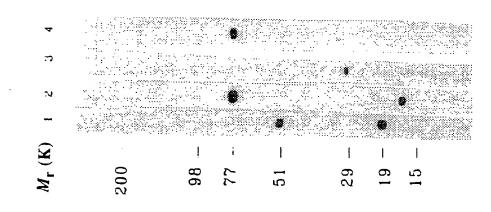
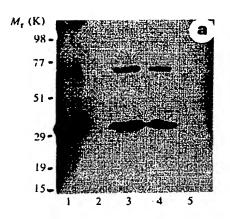
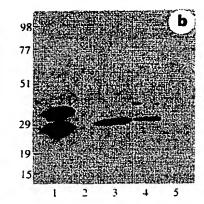


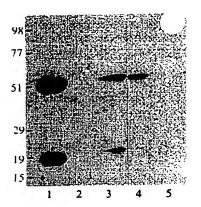
Figure 2

	Clr/Cls —>	
ASP-2	TPLGPKWPEPVFGRLASPGFPGEYANDQERRWTLTAPPGYRLRLYFTHFDLELSHLEEYDFVKLSSGAKVLATLEGQESTDTERAPGKDT	90
(ASP-1	htvelnnmfgqiqspgypdsypsdsevtwnitvpdgfriklyfmhfnlessyl@eydyvkvetedqvlatf@grettdteqtpgqev	87
lr	SIPIPQKLFGEVTSPLFPKPYPNNFETTTVITVPTGYRVKLVFQQFDLEPSEGËFYDYVKISADKKSLGRFËGQLGSPLGNPPGKKE	87
Cls	eptmygeilspnypqaypsevekswdievpegygihlyfthldielsen@aydsvqiisgdteegrl@gqrssnnphspivee	83
	* ** * * * * * * * * * * * * * * * * * *	
IASP-2	FYSLGSSLDITFRSDYSNEKP FTGFEAFYAAEDIDEĞQ VAPGEA PTËDHHËHNHLGGFYĞSËRAGYVLHRNKRTËSALËS	170
ASP-1	VLSPGSFMSITPRSDFSNEER FTGFDAHYMAVDVDECK EREDEE LSCDHYCHNYIGGYYCSCRFGYILHTDNRTCRVECS	167
lr	FMSQGNKMLLTFHTDFSNEENGTIMFYKGFLAYYQAVDLDEÖASRSKSGEEDPQPQÖQHLÖHNYVGGYFÖSÖRPGYELQEDRHSÖQAEÖS	177
18	fovpynklovifksdfsneer ftgfaayyvatdineët dfvd vpëshfënnfiggyfësëppeyflhddmknëgvnës	161
	* * * * * * * * * * * * * * * * * * * *	
	- Clr/Cls>	
ASP-2	GOVFTQRSGELSSPEYPRPYPKLSSÖTYSISLEEGFSVILDFV BSFDVET HPETLÖPYDFLKIQTDREEHGPFÖGKTLPHR IETKS	256
ASP-1	DNLFTQRTGVITSPDFPNPYPKSSECLYTIELEEGFMVNLQFE DIFDIED HPEVPCPYDYIKIKVGPKVLGPFCGEKAPEP ISTQS	253
lr	SELYTEASGYISSLEYPRSYPPDLRÖNYSIRVERGLTLHLKFL EPFDIDD HQQVHÖPYDQLQIYANGKNIGEFÖGKQRPPD LDTSS	263
1s	GDVFTALIGEIASPNYPKPYPENSR©EYQIRLEKGFQVVVTLRREDFDVEAADSAGN© LDSLVFVAGDRQFGPY©GHGFPGPLNIETKS	250
ASP-2	CCP-1> NTVTITFVTDESGDHTGWKIHYTSTAQP@PYPMAPPN GHVSPVQAKYILKDSFSIF@ETGYELLQGHLPLKSFTAV@QKDGSWDRPMPA	345
ASP-1	HSVLILFHSDNSGENRGWRLSYRAAGNECPELQPPVH GKIEPSQAKYFFKDQVLVSCDTGYKVLKDNVEMDTFQIECLKDGTWSNKIPT	342
1r	NAVDLLFFTDESGDSRGWKLRYTTEIIK@PQPKTLDEFTIIQNLQPQYQFRDYFIAT@KQGYQLIEGNQVLHSFTAV@QDDGTWHRAMPR	353
ls	NALDIIFQTDLTGQKKGWKLRYHGDPMPGPKEDTPN SVWEPAKAKYVFRDVVQITGLDGFEVVEGRVGATSFYSTGQSNGKWSNSKLK	338
	* * * ** * ** * * * * * * * * * * * * *	
	CCP-2> Linker>	
ASP-2	ÖSIVDÖGPPDDLPSGR <u>VEYITGPGVTTY</u> KAVIQYSÖEETFYTM KVNDGK <u>YVÖEADGF</u> WTSSKGEKSLPVÖEPVÖGLS ARTT	426
ASP-1	CKIVDCRAPGELEHGLITFSTRNNLTTYKSEIKYSCQEPYYKML NNNTGIYTCSAQGVWMKVLGRSLPTCLPVCGLPKFSRKL	426
lr ls	ÖKIKDÖGQPRNLPNGDFRYTTIMGVNTYKARIQYYÖHEPYYKMQTRAGSRESEQGVYTÖTAQGIWKNEQKGEKIPRÖLPVÖGKPVNPVEQ ÖQPVDÖGIPESIENGKVE DPESTLFGSVIRYTÖEEPYYYME NGGGGEYHÖAGNGSWVNEVLGPELPKÖVPVÖGVPREPFEE	443
15	ÇOPVDÇGIPESIENGKVE DPESTLFGSVIRYTÇEEPYYYME NGGGGEYHÇAGNGSWVNEVLGPELPKÇVPVÇGVPREPFEE	419
ASP-2	GGRIYGGQKAKPGDFPWQVLILGGTTA AGALLYDNWVLTAAH AVYEQKHDASALDIRMGTLKRLSPHYTQAWSEAVFIHEG	507
ASP-1	MARIFNGRPAQKGTTPWIAMLSHLNGQPFCGGSLLGSSWIVTAAHCLHQSLDPKDPTLRDSDLLSPSD FKIILGKHWRLRSDENEQHLG	515
lr	RQRIIGGQKAKMGNFPWQVFTNIHGRG GGALLGDRWILTAAH TLYPKEHEAQSNASLDVFLGHTNVEELMKLGNHP IRRV	523
ls	KQRIIGGSDADIKNFPWQVFFDNPWA GGALINEYWVLTAAH VVEGNREPTMYVGSTSVQTSRLAKSKMLT PEHVFIHPG	498
	** * * **	
ASP-2	YTHDAG FDNDIALIKLNNKVVINSNITPIÖLPRKEAESFMRTDDIGTASGWGLTQRGFLARNLMYVDIPIVDHQKÖTAAYEK	589
ASP-1	VKHTTLHPKYDPNTFENDVALVELLESPVLNAFVMPIČLP EGPQQEGAMVIVSGWGKQFLQRFPETLMEIEIPIVDHSTČQKAY	599
ir	SVHPDYRQDESYN FEGDIALLELENSVTLGPNLLPICLP DNDTFYDLGLMGYVSGFGVMEEK IAHDLRFVRLPVANPQACEN WLR	608
.9	WKLLEV PEGRTN FDNDIALVRLKDPVKMGPTVSPIĞLPGTSSDYNLMDGDLGLISGWGRTEKRDRAVRLKAARLPVAPLRKÖKEVKVE	586
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SP-2	PPYPRG SVTANMLÇAGLESGGKDSÇRGDSGGALVFLDS ETERWFVGGIVSWGSMNÇGEAGQYGVYTKVINYIPWIENIISDF	671
SP-1	APLKK KVTRDMIČAGEKEGGKDAČSGDSGGPMVTLNR ERGQWYLVGTVSWGD DÖGKKDRYGVYSYIHHNKDWIQRVTGVRN	680
ir	GKNRMD VFSQNMFCAGHPSLKQDACQGDSGGVFAVRDP NTDRWVATGIVSWGI GCSRG YGFYTKVLNYVDWIKKEMBEED	688
ls	KPTADAEAYVFTPNMI CAGGEK GMDSCKGDSGGAFAVQDPNDKTKFYAAGLVSWGP QCGT YGLYTRVKNYVDWIMKTMQENSTPRED	673

3/6 Figure 3a

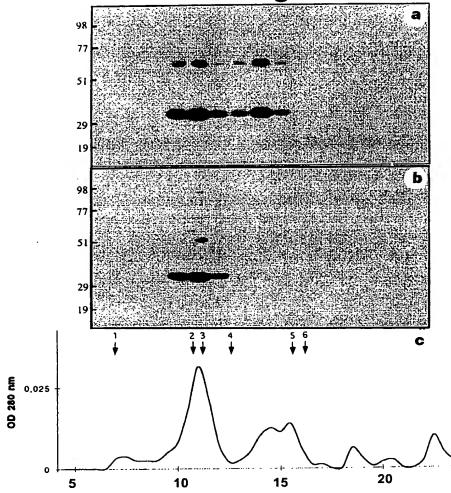




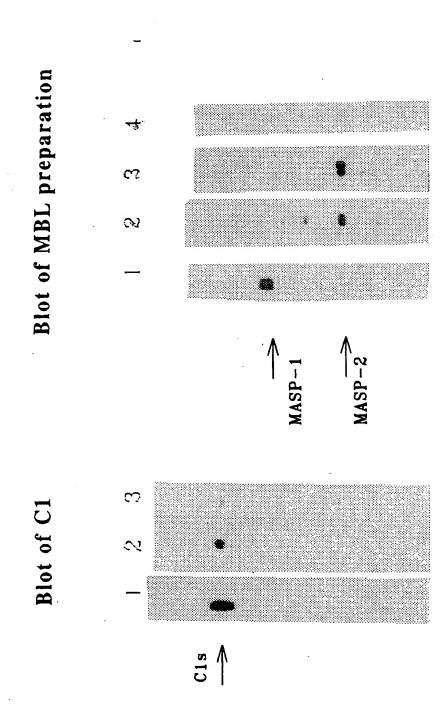


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Figure 3b







COMPACTOR CHOOSE

Figure 5

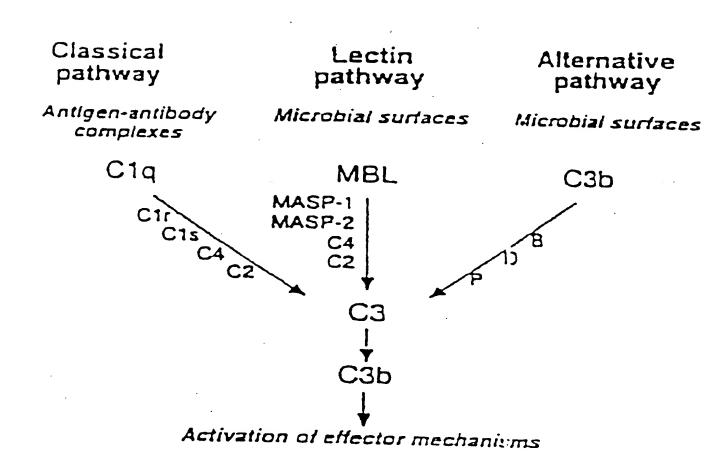


Figure 6

*1	
etegtgelitteggelegaegggelegeleeleeltGAGGTGCTGAGGCTTCTGGCTGGGTGGCTGGGCCACCCCTTAGGCCGAAGT $m{H}$ $m{R}$ $m{L}$ $m{L}$ $m{T}$ $m{L}$ $m{G}$ $m{F}$ $m{K}$	100
GGCCTGAACCTGTGTTCGGGGGCCTGGCATCCCCCGGCTTTCCAGGGGGGTATGCCAACTGACCAGGAGCGGGGGCGCTGGACCCTGACTGCACCCCCGGCTA W P E P V F G R L A S P G F P G E Y A N D O E F R W T L T A P P G Y	200
CONCUTS CONTROL OF THE POLE LS HLCEYDFVKLS CONTROL SGLAND CONTROL OF THE POLE LS HLCEYDFVKLS CONTROL OF A KVLAT	300 73
CTGTGCCCCCAGGAGAGCACAGACACGGAGCGCCCCTGGCAAGGACACTTTCTACTCGCTGCGCCCCCGACCATTACCTTCCGCCTCCGACTACT L C G Q E s T D T E R A P G K D T F Y <u>S L G S S L D I T F R 9 D Y</u>	400 106
COARCGREARCCOTTCACGGGGTTCGAGGGCTTCTATGCAGCCGAGGACATTCACGAGTGCCAGGTGGCCGGGAGAGGGGGCCCACCTGCGACCACCA ${\tt S}$ ${\tt N}$ ${\tt E}$ ${\tt K}$ ${\tt P}$ ${\tt T}$ ${\tt G}$ ${\tt F}$ ${\tt E}$ ${\tt A}$ ${\tt F}$ ${\tt Y}$ ${\tt A}$ ${\tt A}$ ${\tt E}$ ${\tt D}$ ${\tt I}$ ${\tt D}$ ${\tt E}$ ${\tt Q}$ ${\tt V}$ ${\tt I}$ ${\tt P}$ ${\tt G}$ ${\tt E}$ ${\tt A}$ ${\tt P}$ ${\tt T}$ ${\tt C}$ ${\tt D}$ ${\tt H}$ ${\tt H}$	500 140
CCACAACCACCTGGGGGTTTCTACTGCTCCTGCGGGGAGGTACGTCCTGCACCGTAACAACGCCTCTGCTCAGCCCTGTGCTCCGGCAGGTCCCACCTACACACGCCACGTCCCGCCAGGTCCCACACACA	600 173
TTCACCCADAGGTCTGGGGAGCTGAGCAGCCCTGAATACCCACGGCGGTATCCCAACTCTCCAGTTGCACTTACAGCATCAGCCTGGAGGAGGGGTTCA F-T Q R S G E L S S P E Y P R P Y P K L S S C T Y S I S L E E G F	700 206
GTGTCATTCTGGACTTTGTGGAGTCCTTCGATGTGGAGACACACCCTGAAACCCTGTGTCCCTACGACT.TCTCAAGATTCAAACAGACAGAGAAGAACA S V I L D F V E S F D V E T H P E T L C P Y D ? L K I Q T D R E E H	8 0 0 2 4 0
TGGCCCATTCTGTGGGAAGACATTGCCCCACAGGATTGAAACAAAAAGCAACACGGTGACCATCACCTTTGTCACAGAATGAAT	900
TOGAGATCCACTACACCAGCACAGCCCTTGCCCTTATCCCATGCCCCAATGGCCAACGTTTCACCTCTGCAAGCCAAATACATCCTGAAAG W K I H Y T S T A Q P C P Y P H A P P N G H V S P V Q A K Y I L K	306
ACAGCTTCTCCATCTITICCCACACTGGCTATGAGCTTCTGCAAGGTCACTTGCCCCTGAAATCCTTTATGCAGTTTGTCAGAAAGATGGATCTTGCGA D S F S I F C E T G Y E L L Q G B L P L X S F I A V C Q K D G S W D	340
R P M P A C S I V D C G P P D D L P S G R V E Y I T G P G V T T Y	1200
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